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<b>References</b>	
[ 1] Futai M., Noumi T., Maeda M. Annu. Rev. Biochem. 58:111-136(1989).	
[ 2] Senior A.E. Physiol. Rev. 68:177-231(1988).	
[ 3] Miki J., Maeda M., Mukohata Y., Futai M. FEBS Lett. 232:221-226(1988).	
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## General information about the entry

Entry name	ATPG_ECOLI
Primary accession number	P00837
Secondary accession number	P00838
Entered in Swiss-Prot in	Release 01, July 1986
Sequence was last modified in	Release 01, July 1986
Annotations were last modified in	Release 42, September 2003
<b>Name and origin of the protein</b>	
Protein name	ATP synthase gamma chain
Synonym	EC <u>3.6.3.14</u>
Gene name	ATPG or UNCG or PAPC or <u>B3733</u> or <u>C4659</u> or <u>Z5231</u> or ECS4675 or SF3813
From	<u>Escherichia coli</u> [TaxID: <u>562</u> ] <u>Escherichia coli O6</u> [TaxID: <u>217992</u> ] <u>Escherichia coli O157:H7</u> [TaxID: <u>83334</u> ] <u>Shigella flexneri</u> [TaxID: <u>623</u> ]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Escherichia</u> .

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
SPECIES=E.coli;  
MEDLINE=85121806; PubMed=6395859; [NCBI, ExPASy, EBI, Israel, Japan]  
Walker J.E., Gay N.J., Saraste M., Eberle A.N.;  
"DNA sequence around the Escherichia coli unc operon. Completion of the sequence of a 17 kilobase segment containing asnA, oriC, unc, glmS and phoS."  
Biochem. J. 224:799-815(1984).
- [2] SEQUENCE FROM NUCLEIC ACID.  
SPECIES=E.coli;  
MEDLINE=82059507; PubMed=6272217; [NCBI, ExPASy, EBI, Israel,

	<p><u>Japan]</u></p> <p><u>Saraste M., Gay N.J., Eberle A., Runswick M.J., Walker J.E.:</u>          "The atp operon: nucleotide sequence of the genes for the gamma, beta, and epsilon subunits of Escherichia coli ATP synthase."  <u>Nucleic Acids Res. 9:5287-5296(1981).</u></p>
[3]	<p>SEQUENCE FROM NUCLEIC ACID.  <b>SPECIES</b>=E.coli;          MEDLINE=82134798; PubMed=6277310; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u>  <u>Kanazawa H., Kayano T., Mabuchi K., Futai M.:</u>          "Nucleotide sequence of the genes coding for alpha, beta and gamma subunits of the proton-translocating ATPase of Escherichia coli."  <u>Biochem. Biophys. Res. Commun. 103:604-612(1981).</u></p>
[4]	<p>SEQUENCE FROM NUCLEIC ACID.  <b>SPECIES</b>=E.coli;  <b>STRAIN</b>=K12 / MG1655;          MEDLINE=93315143; PubMed=7686882; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u>  <u>Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.:</u>          "DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication."  <u>Genomics 16:551-561(1993).</u></p>
[5]	<p>SEQUENCE FROM NUCLEIC ACID.  <b>SPECIES</b>=E.coli;  <b>STRAIN</b>=O6:H1 / CFT073 / ATCC 700928;          MEDLINE=22388234; PubMed=12471157; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u>  <u>Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.:</u>          "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."  <u>Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).</u></p>
[6]	<p>SEQUENCE FROM NUCLEIC ACID.</p>

	<p><b>SPECIES</b>=E.coli;</p> <p><b>STRAIN</b>=O157:H7 / EDL933 / ATCC 700927;</p> <p><b>MEDLINE</b>=21074935; PubMed=11206551; [<a href="#">NCBI</a>, <a href="#">ExPASy</a>, <a href="#">EBI</a>, <a href="#">Israel</a>, <a href="#">Japan</a>]</p> <p><a href="#">Perna N.T.</a>, <a href="#">Plunkett G. III</a>, <a href="#">Burland V.</a>, <a href="#">Mau B.</a>, <a href="#">Glasner J.D.</a>, <a href="#">Rose D.J.</a>, <a href="#">Mayhew G.F.</a>, <a href="#">Evans P.S.</a>, <a href="#">Gregor J.</a>, <a href="#">Kirkpatrick H.A.</a>, <a href="#">Posfai G.</a>, <a href="#">Hackett J.</a>, <a href="#">Klink S.</a>, <a href="#">Boutin A.</a>, <a href="#">Shao Y.</a>, <a href="#">Miller L.</a>, <a href="#">Grotbeck E.J.</a>, <a href="#">Davis N.W.</a>, <a href="#">Lim A.</a>, <a href="#">Dimalanta E.T.</a>, <a href="#">Potamousis K.</a>, <a href="#">Apodaca J.</a>, <a href="#">Anantharaman T.S.</a>, <a href="#">Lin J.</a>, <a href="#">Yen G.</a>, <a href="#">Schwartz D.C.</a>, <a href="#">Welch R.A.</a>, <a href="#">Blattner F.R.</a>;</p> <p>"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";</p> <p>Nature 409:529-533(2001).</p>
[7]	<p>SEQUENCE FROM NUCLEIC ACID.</p> <p><b>SPECIES</b>=E.coli;</p> <p><b>STRAIN</b>=O157:H7 / RIMD 0509952;</p> <p><b>MEDLINE</b>=21156231; PubMed=11258796; [<a href="#">NCBI</a>, <a href="#">ExPASy</a>, <a href="#">EBI</a>, <a href="#">Israel</a>, <a href="#">Japan</a>]</p> <p><a href="#">Hayashi T.</a>, <a href="#">Makino K.</a>, <a href="#">Ohnishi M.</a>, <a href="#">Kurokawa K.</a>, <a href="#">Ishii K.</a>, <a href="#">Yokoyama K.</a>, <a href="#">Han C.-G.</a>, <a href="#">Ohtsubo E.</a>, <a href="#">Nakayama K.</a>, <a href="#">Murata T.</a>, <a href="#">Tanaka M.</a>, <a href="#">Tobe T.</a>, <a href="#">Iida T.</a>, <a href="#">Takami H.</a>, <a href="#">Honda T.</a>, <a href="#">Sasakawa C.</a>, <a href="#">Ogasawara N.</a>, <a href="#">Yasunaga T.</a>, <a href="#">Kuhara S.</a>, <a href="#">Shiba T.</a>, <a href="#">Hattori M.</a>, <a href="#">Shinagawa H.</a>;</p> <p>"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";</p> <p>DNA Res. 8:11-22(2001).</p>
[8]	<p>SEQUENCE OF <u>261-287</u> FROM NUCLEIC ACID.</p> <p><b>SPECIES</b>=E.coli;</p> <p><b>MEDLINE</b>=90202983; PubMed=2138624; [<a href="#">NCBI</a>, <a href="#">ExPASy</a>, <a href="#">EBI</a>, <a href="#">Israel</a>, <a href="#">Japan</a>]</p> <p><a href="#">Iwamoto A.</a>, <a href="#">Miki J.</a>, <a href="#">Maeda M.</a>, <a href="#">Futai M.</a>;</p> <p>"H(+)-ATPase gamma subunit of Escherichia coli. Role of the conserved carboxyl-terminal region.";</p> <p>J. Biol. Chem. 265:5043-5048(1990).</p>
[9]	<p>SEQUENCE FROM NUCLEIC ACID.</p> <p><b>SPECIES</b>=S.flexneri;</p> <p><b>STRAIN</b>=301 / Serotype 2a;</p> <p><b>MEDLINE</b>=22272406; PubMed=12384590; [<a href="#">NCBI</a>, <a href="#">ExPASy</a>, <a href="#">EBI</a>, <a href="#">Israel</a>,</p>

	<p><u>Japan]</u></p> <p><u>Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.;</u></p> <p>"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).</p>
[10]	<p>X-RAY CRYSTALLOGRAPHY (4.4 ANGSTROMS).</p> <p><b>SPECIES</b>=E.coli;</p> <p>MEDLINE=20040613; PubMed=10570135; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u></p> <p><u>Hausrath A.C., Grueber G., Matthews B.W., Capaldi R.A.;</u></p> <p>"Structural features of the gamma subunit of the Escherichia coli F(1) ATPase revealed by a 4.4-A resolution map obtained by X-ray crystallography."; Proc. Natl. Acad. Sci. U.S.A. 96:13697-13702(1999).</p>

## Comments

**FUNCTION:** PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.

**CATALYTIC ACTIVITY:**  $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$ .

**SUBUNIT:** F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

**SIMILARITY:** Belongs to the ATPase gamma chain family.

**CAUTION:** REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS AND VARIOUS OTHER ERRORS.

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## Cross-references

EMBL	X01631; CAA25781.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	J01594; AAA24736.1; [EMBL / GenBank / DDBJ] ALT_FRAME. [CoDingSequence]
	V00267; CAA23526.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	M25464; AAA83874.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	V00312; CAA23597.1; [EMBL / GenBank / DDBJ] ALT_FRAME. [CoDingSequence]
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	AE000450; AAC76756.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
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	AE005605; AAG58936.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
	AP002566; BAB38098.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
	M34095; AAA24742.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE015388; AAN45253.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
PIR	A01038; PWECG. C91213; C91213. D86059; D86059.
PDB	1D8S; 03-DEC-99. [ExPASy / RCSB] 1FS0; 01-MAY-01. [ExPASy / RCSB] <u>Detailed list of linked structures.</u>

EcoGene	<a href="#">EG10104</a> ; atpG.
EcoCyc	<a href="#">EG10104</a> ; atpG.
CMR	<a href="#">P00837</a> ; B3733.
InterPro	<a href="#">IPR000131</a> ; ATPase_gamma. <a href="#">Graphical view of domain structure.</a>
Pfam	<a href="#">PF00231</a> ; ATP-synt; 1.
PRINTS	<a href="#">PR00126</a> ; ATPASEGAMMA.
TIGRFAMs	<a href="#">TIGR01146</a> ; ATPsyn_F1gamma; 1.
PROSITE	<a href="#">PS00153</a> ; ATPASE_GAMMA; 1.
ProDom	<a href="#">[Domain structure / List of seq. sharing at least 1 domain]</a>
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### Keywords

[ATP synthesis](#); [CF\(1\)](#); [Hydrogen ion transport](#); [Hydrolase](#); [3D-structure](#); [Complete proteome](#).

### Features

None

### Sequence information

Length: 287 AA	Molecular weight: 31577 Da	CRC64: 2417A4B8FBDB8EF8 [This is a checksum on the sequence]
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130	140	150	160	170	180
KGVSTFFNSVG	GNVVAQVTGM	GDNPSSLSELI	GPVKVMLQAY	DEGRDLDKLYI	VSNKFINTMS
190	200	210	220	230	240
QVPTISQLLP	LPASDDDDLK	HKSWDYLYEP	DPKALLDTLL	RRYVESQVYQ	GVVENLASEQ
250	260	270	280		
AARMVAMKAA	TDNGGSLIKE	LQLVYNKARQ	ASITQELTEI	VSGAAAV	

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 289 AA

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Program: NCBI BLASTP 2.2.5 [Nov-16-2002]

Database: XXtremblnew; XXtrembl; XXswissprot

1,135,895 sequences; 361,048,751 total letters

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<input type="checkbox"/> sp <a href="#">Q9L6B6</a>	ATPG_PASMU ATP synthase gamma chain (EC 3.6.3.14) [ATP...	555	e-157
<input type="checkbox"/> sp <a href="#">P43716</a>	ATPG_HAEIN ATP synthase gamma chain (EC 3.6.3.14) [ATP...	456	e-127
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<input type="checkbox"/>	tn <a href="#">AAP19743</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">228</a>	9e-59
<input type="checkbox"/>	tn <a href="#">AAP19759</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">227</a>	1e-58
<input type="checkbox"/>	tn <a href="#">AAP19752</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">227</a>	1e-58
<input type="checkbox"/>	tn <a href="#">AAP19745</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">227</a>	1e-58
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<input type="checkbox"/>	tn <a href="#">AAP19742</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">226</a>	2e-58
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<input type="checkbox"/>	tn <a href="#">AAP19753</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">226</a>	2e-58
<input type="checkbox"/>	tn <a href="#">AAP19751</a>	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...	<a href="#">226</a>	2e-58
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<input type="checkbox"/>	sp	<a href="#">P37810</a>	ATPG_BACSU ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">207</a>	9e-53
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<input type="checkbox"/>	tn	<a href="#">AAP29192</a>	ATP synthase F1, gamma subunit [atpG] [Bacillus anth...	<a href="#">207</a>	2e-52
<input type="checkbox"/>	tr	<a href="#">Q8E5U9</a>	H+-transporting ATP synthase gamma chain [ATPG] [Strep...	<a href="#">205</a>	6e-52
<input type="checkbox"/>	tn	<a href="#">AAO82318</a>	ATP synthase F1, gamma subunit [atpG] [Enterococcus ...	<a href="#">205</a>	6e-52
<input type="checkbox"/>	tr	<a href="#">Q9RAU1</a>	H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase...	<a href="#">204</a>	1e-51
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<input type="checkbox"/>	tr	<a href="#">O05432</a>	ATP synthase subunit gamma [ATPG] [Moorella thermoacet...	<a href="#">201</a>	7e-51
<input type="checkbox"/>	tr	<a href="#">O50158</a>	Proton-translocating ATPase, gamma subunit [ATPG] [Str...	<a href="#">201</a>	1e-50
<input type="checkbox"/>	tr	<a href="#">Q8EM82</a>	H(+)-transporting ATP synthase gamma chain (EC 3.6.1.3...	<a href="#">197</a>	9e-50
<input type="checkbox"/>	tr	<a href="#">Q9A0I8</a>	Putative proton-translocating ATPase, gamma subunit (E...	<a href="#">197</a>	9e-50
<input type="checkbox"/>	sp	<a href="#">P09222</a>	ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6....	<a href="#">196</a>	2e-49
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<input type="checkbox"/>	tr	<a href="#">Q927W3</a>	AtpG protein [ATPG] [Listeria monocytogenes, Listeria ...	<a href="#">193</a>	2e-48
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<input type="checkbox"/>	sp	<a href="#">P41010</a>	ATPG_BACCA ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">190</a>	2e-47
<input type="checkbox"/>	sp	<a href="#">P29710</a>	ATPG_PROMO ATP synthase gamma chain, sodium ion specif...	<a href="#">189</a>	3e-47
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<input type="checkbox"/>	sp	<a href="#">Q06908</a>	ATPG_ODOSI ATP synthase gamma chain, chloroplast precu...	<a href="#">187</a>	1e-46
<input type="checkbox"/>	tr	<a href="#">Q9ZJ02</a>	Proton-translocating ATPase gamma subunit [Streptococc...	<a href="#">187</a>	2e-46
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<input type="checkbox"/>	tr	<a href="#">Q8KRU9</a>	Subunit gamma [ATPG] [Ilyobacter tartaricus]	<a href="#">184</a>	8e-46
<input type="checkbox"/>	tr	<a href="#">Q8RGE1</a>	ATP synthase gamma chain, sodium ion specific (EC 3.6....	<a href="#">184</a>	1e-45
<input type="checkbox"/>	sp	<a href="#">Q41075</a>	ATPG_PHATR ATP synthase gamma chain, chloroplast precu...	<a href="#">183</a>	2e-45
<input type="checkbox"/>	sp	<a href="#">Q10597</a>	ATPG_MYCTU ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">182</a>	4e-45
<input type="checkbox"/>	sp	<a href="#">P56082</a>	ATPG_HELPHY ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">181</a>	7e-45
<input type="checkbox"/>	sp	<a href="#">Q9ZK80</a>	ATPG_HELPIJ ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">179</a>	3e-44
<input type="checkbox"/>	sp	<a href="#">P50006</a>	ATPG_SPIPL ATP synthase gamma chain (EC 3.6.3.14) [ATP...	<a href="#">179</a>	3e-44
<input type="checkbox"/>	tr	<a href="#">Q8A9U6</a>	ATP synthase gamma chain [BT0719] [Bacteroides thetaio...	<a href="#">178</a>	6e-44

Graphical overview of the alignments

Click here

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(use ScanProsite for more details about PROSITE matches)

new

Profile hits		
Pfam hits	ATP	
Submission	Matches on query sequence	Matcl
	1 50 100 150 200 250	1
ATPG_PASMU		
ATPG_HAEIN		
Q9KNH4		
ATPG_ECOLI		
Q9RFL4		
RAAP18944		
Q8Z9S5		
Q8ZKN8		
Q8E8B9		
Q8DDG9		
Q8Z2Q5		
RAA071150		
ATPG_VIBAL		
Q87KA7		
Q8VV78		
Q9HT19		
Q88BX3		
Q87TT3		
Q8XU75		
CA084116		
RAA091434		
Q8PCZ6		
Q8PGG6		
ATPG_BUCAI		
ATPG_THIFE		
ATPG_BUCAP		
Q9PE84		
Q87E89		
Q9JM71		
Q9JXQ1		
Q9RQ80		
Q8D3J4		
Q9RQ74		
Q89B40		
Q9RQ77		
RAAP19756		
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RAAP19757		
RAAP19755		
RAAP19743		
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RAAP19761		
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RAAP19754		
RAAP19753		
RAAP19751		
RAAP19749		
RAAP19748		
RAAP19747		
RAAP19746		
RAAP19750		
RAAP19758		
ATPG_BACME		
ATPG_BACFI		
ATPG_BACHD		
ATPG_BACSU		
RAAP12170		
RAAP29192		
Q8E5U9		
RAA082318		
Q9RAU1		
ATPG_LACLA		
Q8E073		
Q05432		
Q050158		

\_PCL XL error

Subsystem: KERNEL

Error: IllegalOperatorSequence

Operator: SetClipToPage

Position: 9096

# IPB000131: ATPase\_gamma

## ATP synthase gamma subunit

- [Introduction](#)
- [Block number IPB000131A](#)
- [Block number IPB000131B](#)
- [Block number IPB000131C](#)
- [Block number IPB000131D](#)
- [Block number IPB000131E](#)
- InterPro entry [IPR000131](#) (source of sequences used to make blocks)
- Block Maps. [\[Graphical Map\]](#) [\[Text Map\]](#) [\[Map Positions\]](#) [\[About Maps\]](#)
- Logos. [\[About Logos\]](#)  
Select display format: [\[GIF\]](#) [\[PDF\]](#) [\[Postscript\]](#)
- Tree from blocks alignment. [\[About Trees\]](#) [\[About ProWeb TreeViewer\]](#)  
[\[Data\]](#) [\[ProWeb TreeViewer\]](#) [\[XBitmap\]](#) [\[GIF\]](#) [\[PDF\]](#) [\[Postscript\]](#)  
[\[Newick\]](#)
- [Structures](#)
- Search blocks vs other databases:
  - [COBBLER sequence](#) and BLAST searches [\[About COBBLER\]](#)
  - [MAST Search](#) of all blocks vs a sequence database [\[About MAST\]](#)
  - [LAMA search](#) of all blocks vs a blocks database [\[About LAMA\]](#)
- [CODEHOP](#) to design PCR primers from blocks [\[About CODEHOP\]](#)
- [SIFT](#) to predict amino acid substitutions in blocks [\[About SIFT\]](#)

## ◦ Additional Links

[\[Return to top\]](#)

## Block IPB000131A

```

ID    ATPase_gamma; BLOCK
AC    IPB000131A; distance from previous block=(0,62)
DE    ATP synthase gamma subunit
BL    ITM; width=32; seqs=82; 99.5%=1504; strength=1376
ATPG  MYCGA|P33257 ( 4) MQDLKRRMESITVTHKITKAMKMLSTVKLNRF 53
ATPG  PROMO|P29710 ( 3) GKEIKSRISVQSTRQITKAMEIVSSTKFKKF 22
ATPG  RHORU|P07227 ( 4) LKDLRSRITSVKSTQKITSAMKMVAASRLRRA 10
ATPG  RICPR|O50289 ( 4) LKQLRTRIKSVKSTQKITKAMQLVSASKMTKI 12
ATPG  ANASP|P12408 ( 4) LKSIRDRIQSVKNTKKITEAMRLVAAARVRR 14
ATPG  RHOBL|P05436 ( 4) LKDLKNRIGSVKNTRKITKAMQMVAAAKLRR 8
ATPG  RHOCA|P72246 ( 4) LKDLKNRIVSVKNTRKITKAMQMVAAANIRRA 15
ATPG  SPIPL|P50006 ( 3) LKAIRDRIQSVKNTKKITEAMRLVASAKVRR 10
ATPG  SYNPF|Q05384 ( 4) LKAIRDRIKTIKDTRKITEAMRLVAAAKVRR 17
ATPG  SYNPF|P08450 ( 4) LKAIRDRIKSVNTRKITEAMRLVAAAKVRR 13
ATPG  SYNPF|P17253 ( 4) LKAIRDRIQSVKNTKKITEAMRLVAAAKVRR 9
ATP1  ARATH|Q01908 ( 53) LRELDRIDSVKNTQKITEAMKLVAAGVRR 8
ATP2  ARATH|Q01909 ( 63) IRELDRIDSVKNTQKITEAMRLVAAARVRR 12
ATPG  CHLRE|P12113 ( 37) LKEVRDRIASVKNTQKITDAMKLVAAGVRR 12
ATPG  ODOSE|Q06908 ( 59) ANAIRDRIQSVKNTKKITMAMKLVAAGVRR 11
ATPG  PEA|P28552 ( 54) LKDLKNRIDSVKNTQKITEAMKLVAAGVRR 8
ATPG  PHATR|Q41075 ( 58) ANAIRDRIQSVKNTRKITMAMKLVAAPKVR 43
ATPG  SPIOL|P05435 ( 44) LRELDRIGSVKNTQKITEAMKLVAAGVRR 8
ATPG  TOBAC|P29790 ( 57) LRDLRDRIESVKNTQKITEAMKLVAAGVRR 8

ATPG  BACCA|P41010 ( 7) LRDIKTRINATKKTSQITKAMEMVSTSKLNRA 10
ATPG  BACFI|P22482 ( 4) LRDIQGRITSTKTKQITKAMQMVSAAKLNRA 12
ATPG  BACP3|P09222 ( 7) LRDIKTRINATKKTSQITKAMEMVLTSLNRA 15

ATPG  BUCAI|P57123 ( 4) TKEIKNKIVSVTNTKKITKAMEMVAASKMRKT 12
ATPG  BUCAP|O51873 ( 4) KKEIKDQIIISVTNTKKITKAMEMVAASKMRKT 17

ATPG  ECOLI|P00837 ( 4) AKEIRSKIASVQNTQKITKAMEMVAASKMRKS 8
ATPG  THIFE|P41169 ( 4) AKEIRGQIKSVKNTRKITRAMEMVAASKMRRA 12
ATPG  VIBAL|P12990 ( 4) AKEIRNKIGSVKSTQKITKAMEMVAASKMRRS 8

ATPG  MYCGE|P47640 ( 4) IQEIKRRMNTVKSTIKITNAMKMVSRAKFIK 26
ATPG  MYCPN|Q50330 ( 4) IQEIKRKMNTVQSTIKITNAMKMVSRAKFVR 22

ATP3  ARATH|Q96250 ( 45) TQVVRNRMKSVKNIQKITKAMKMVAASKLRAV 24
ATP3  IPOBA|P26360 ( 48) TQVVRNRMKSVKNIQKITKAMKMVAASKLRAI 20

ATPG  BOVIN|P05631 ( 28) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13
ATPG  HUMAN|P36542 ( 28) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13
ATPG  RAT|P35435 ( 3) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13

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ATPG_KLULA	P49377	( 20)	LREIETRLKSIKNIKITKTMKIVASTRLSKA	24
ATPG_YEAST	P38077	( 36)	LKEVEMRLKSIKNIKITKTMKIVASTRLSKA	28
ATPG_ACEWO	P50005	( 4)	VQDIKPRIKSVNSTMQITHAMELVASAKLRKS	21
ATPG_BACME	P20602	( 4)	LRDIQTRITSTKKTSSQITKAMEMVSAAKLNRA	11
ATPG_BACST	P42007	( 7)	LRDIKTRINATKKTSSQITKAMEMVSTSKLNRA	10
ATPG_BACSU	P37810	( 7)	LRDIKSRTSTKKTSSQITKAMQMVSAAKLNRA	9
ATPG_ENTHR	P43452	( 5)	LNEIKTRIASTKKTSSQITRAMQMVSAASKLTKS	11
ATPG_HAEIN	P43716	( 4)	AKEIKTKIASVQSTQKITKAMEMVATSKMRKT	8
ATPG_HELPI	P56082	( 4)	LRDIRKKIGSVKNTQKITHAMKLVSTSKLRKA	10
ATPG_HELPI	P56082	( 4)	LRDIRKKIGSVKNTQKITHAMKLVSTSKLRKA	14
ATPG_MYCLE	P45824	( 5)	LRELGRIRSVSGSIKKITKAQELIATSRIARA	18
ATPG_MYCTU	P45824	( 5)	LRELGRIRSVSGSIKKITKAQELIATSRIARA	27
ATPG_PASMU	P9L6B6	( 4)	AKEIRTKIASVKSTQKITKAMEMVAASKMRKT	8
ATPG_STRLI	P50007	( 4)	LRVYKRRIRSVTATKKITKAMEMIAASRVVKA	17
ATPG_STRMU	P95788	( 5)	LSEIKVRITSTQKTGKITSAMKMWSSAKLVKS	20
ATPG_DROME	O01666	( 29)	LKMISIRLKSIVKNIQKITQSMKMWSSAKLVKS	32
O74754		( 34)	LKEIEQRLKSIKNIKITKTIKTVAQTKLTRA	38
Q9NE84		( 5)	LRLYKEKLEGYNRFYSIVKTIKMTMAKFRQA	100
O21267		( 4)	TKDFKNRIKSITSIRKITKAMKMWSSAKLRQA	20
Q9G8R3		( 4)	PKKLLKQLKSYERFKLLTKAIQMVVALSQLSGL	93
O50141		( 4)	MKDVKRRIKSVESTMQITKAMQLVASSKMRKA	14
O50158		( 5)	LSEIKGKIISTQKTSHITGAMQMVSAAKLTKS	20
O67829		( 6)	PRDIKRKIQGIKNTKRTITNAMKVVSAAKLRKA	27
O05432		( 4)	MRDLKRRIRSVQSTQHITRAMKMWAAAKLRKA	13
Q52412		( 3)	LRDIKTRINATKKTSSQITKAMEMVLTSKLNRA	15
Q9ZJ02		( 5)	LNDIKNKIASTKNTSQITNAMQMVSAAKLGKS	15
Q9Z688		( 6)	LI I I K R R I K S I T N T K K I T N A M G L I A T S N L R K S	35
Q9X1U6		( 1)	MLQIKRKINATQSLMKITRAMEMVARAKVRKI	33
Q9RQ80		( 4)	IKKIKTQITSVVNTKKITKAMEMVAISKMRKT	18
Q9RQ77		( 4)	KKEIKNKINCISNTKKITKAMEMVSIKMKKS	22
Q9RQ74		( 4)	IKKIKNKIKCITNTQKITKAMEMVSIKMKKA	17
Q9RGY2		( 5)	LLELKRKIASVKQTGKITEAMRMVSASKLNQT	22
Q9RFL4		( 4)	AKEIRSKIASVQNTQKITKAMEMVAASKMRKS	8
Q9RAU1		( 5)	LNEIKTKIASTKKTSSQITGAMQMVSAAKLQKA	13
Q9PR14		( 3)	LDAMKRKINSVQTTAKITNAMKLVATAKLKRQ	38
Q9PJ20		( 4)	LKEIKRKIKSVHNTQKTITNAMKLVSTAKLKKA	25
Q9PE84		( 4)	GREIKSKIKSVQNTKRVTRALEMVSASKIRKA	34
Q9KNH4		( 4)	AKEIRTKIGSVKSTQKITKAMEMVAASKMRRS	8
Q9K6H4		( 4)	LRDIKQRINSTKKTQKITKAMEMVSAAKLNRS	10
Q9K4D4		( 5)	LRVYKRRIRSVTATKKITKAMEMIAASRVVKA	17
Q9JXQ1		( 4)	GKEILTKIRSVQNTQKITKAMQMVSTSKMRKT	12
Q9JW71		( 4)	GKEILTKIRSVQNTQKITKAMQMVSTSKMRKT	12
Q9HT19		( 4)	AKEIRSKIASIKSTQKITNAMEKVAVSKMRKA	18
Q9FDR6		( 4)	IRELRDRIRSVNSTKKITKAQELIATSRIITKA	16
Q9FAA4		( 4)	IRELRDRIRSVNSTKKITKAQELIATSRIITKA	16
Q9CER9		( 5)	LNEIKTKIASTKKTSSQITGAMQMVSAAKLQKA	13
Q9ERA8		( 28)	LKDITRRLKSIKNIQKITKSMKMWAAAKYARA	13
Q9D9D7		( 28)	LKDITRRLKSIKNIQKITKSMKMWAAAKYARA	13

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[\[Return to top\]](#)

## Block IPB000131B

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DE ATP synthase gamma subunit  
BL DGL; width=25; seqs=82; 99.5%=1302; strength=1268  
ATPG\_BACFI|P22482 ( 73) VKKTGYIVVTSKGLAGGYNSSLIR 9  
ATPG\_MYCGA|P33257 ( 74) STKRLWIVINTQLGLCGSYNTNVGK 49

<u>ATPG PROMO</u>	<u>P29710</u>	( 73)	VKRIGIIVMTSDRGLCGGFNSSTLK	12
<u>ATPG RHOBL</u>	<u>P05436</u>	( 74)	DQIHLLVMTSERGLCGGFNSTIVR	23
<u>ATPG RHOCA</u>	<u>P72246</u>	( 76)	DKVHLLVIMTGERGLCGGFNANIAK	20
<u>ATPG RHORU</u>	<u>P07227</u>	( 76)	DNVHLIVALTANRGLCGGFNGSIIR	24
<u>ATPG RICPR</u>	<u>O50289</u>	( 77)	SKINLLIVMTSERGLCGMFNYSIIK	32
<u>ATPG SPIPL</u>	<u>P50006</u>	( 74)	VKKVGLVVLAGNRGLCGAYNSNIIK	19
<u>ATPG THIFE</u>	<u>P41169</u>	( 73)	VKKAGFLVVTDDRGLCGGLNVNVL	12
<u>ATPG ANASP</u>	<u>P12408</u>	( 75)	VKSVGLLVISGDRGLCGGYNTNVIR	11
<u>ATPG SYNPI</u>	<u>Q05384</u>	( 75)	VKTVALLVVTGDRGLCGGYNTNVIR	11
<u>ATPG SYNPI</u>	<u>P08450</u>	( 75)	VKTVALLVVSGDRGLCGGYNSNVIR	11
<u>ATPG SYNPI</u>	<u>P17253</u>	( 75)	PKAVALLVVTGDRGLCGGYNVNAIK	26
<u>ATPG BACCA</u>	<u>P41010</u>	( 73)	VKKTGYLVITSRGLAGAYNSNVVR	9
<u>ATPG BACPI</u>	<u>P09222</u>	( 74)	VKKTGYLVITSRGLAGAYNSNVLR	9
<u>ATPG BUCAI</u>	<u>P57123</u>	( 73)	TNRIGMIIISTDRGLCGGLNTNLFK	16
<u>ATPG BUCAP</u>	<u>O51873</u>	( 73)	DKRIGIIIVSTDRLCGSLNTNLFK	12
<u>ATPG ECOLI</u>	<u>P00837</u>	( 73)	VKRVGYLVVSTDRLCGGLNINLFK	10
<u>ATPG VIBAL</u>	<u>P12990</u>	( 73)	AKRVGYIIVSTDRLCGGLNINVFK	11
<u>ATPG MYCGE</u>	<u>P47640</u>	( 69)	NQKTLWIMMSSSLGCGQHNSNMNK	39
<u>ATPG MYCPN</u>	<u>Q50330</u>	( 69)	NPKTLWVMMSSSLGCGQHNTNMNK	39
<u>ATP1 ARATH</u>	<u>Q01908</u>	( 124)	VKKVALVVVTGDRGLCGGFNNFIIK	11
<u>ATP2 ARATH</u>	<u>Q01909</u>	( 134)	VKRVALVVVTGDKGLCGGFNNAVTK	18
<u>ATPG CHLRE</u>	<u>P12113</u>	( 108)	VKSVLLVLTGDRGLCGGYNNFIIK	14
<u>ATPG PEA</u>	<u>P28552</u>	( 125)	VKKVALVVCCTGDRGLCGGFNNAILK	17
<u>ATPG SPIOL</u>	<u>P05435</u>	( 115)	VKKVALMVVTGDRGLCGGFNNMLLK	30
<u>ATPG TOBAC</u>	<u>P29790</u>	( 128)	VKKVALVVVTGDRGLCGGFNNYLIK	15
<u>ATPG ODOSI</u>	<u>Q06908</u>	( 130)	VSKVTLVVITGDRGLCGGYNSFMIK	17
<u>ATPG PHATR</u>	<u>Q41075</u>	( 130)	VKKVTLVVITGDRGLCGGYNSFMIK	15
<u>ATP3 ARATH</u>	<u>Q96250</u>	( 102)	VKKSVMVTLSSDKGLCGGINSTVVK	20
<u>ATP3 IPOBA</u>	<u>P26360</u>	( 105)	VKKNVIIITISSDKGLCGGINSTSVK	21
<u>ATPG BOVIN</u>	<u>P05631</u>	( 88)	KKKHLLIIGVSSDRGLCGAIHSSVAK	14
<u>ATPG HUMAN</u>	<u>P36542</u>	( 88)	KKKHLLIIGVSSDRGLCGAIHSSIAK	14
<u>ATPG RAT</u>	<u>P35435</u>	( 63)	KKKHLLIIGVSSDRGLCGAIHSSVAK	14
<u>ATPG KLULA</u>	<u>P49377</u>	( 81)	EKKDLIIAITSKGLCGSIHSQLAK	20
<u>ATPG YEAST</u>	<u>P38077</u>	( 102)	APKELIVAITSDKGLCGSIHSQLAK	25
<u>ATPG ACEWO</u>	<u>P50005</u>	( 73)	VKKTAYIIITGDKGLAGGYNVNVAK	11
<u>ATPG BACME</u>	<u>P20602</u>	( 73)	VKKTGYIVITSRGLAGAYNSNIIK	9
<u>ATPG BACST</u>	<u>P42007</u>	( 73)	VKKTGYLVITSRGLAGAYNSNVVR	9
<u>ATPG BACSU</u>	<u>P37810</u>	( 76)	VKKTAYLVITSRGLAGAFNSSVLR	9
<u>ATPG ENTHR</u>	<u>P43452</u>	( 85)	VKKTGYIVITADGGLVGGYNSIILK	22
<u>ATPG HAEIN</u>	<u>P43716</u>	( 73)	VKKIGILVISTDRGMCGGLNVNLFK	15
<u>ATPG HELPY</u>	<u>P56082</u>	( 81)	IKKVDIIFITADKGLCGGFNTNTIK	16
<u>ATPG HELPJ</u>	<u>Q9ZK80</u>	( 81)	IKKVDIIFITADKGLCGGFNTNTIK	16
<u>ATPG MYCLE</u>	<u>P45824</u>	( 74)	PKRAGVLVVSSDRGLCGAYNANVFR	11
<u>ATPG MYCTU</u>	<u>Q10597</u>	( 74)	PKRAGVLVVSSDRGLCGAYNANIFR	11
<u>ATPG PASMU</u>	<u>Q9L6B6</u>	( 73)	VKKVGMIVVSTDRLCGGLNVNLFK	12
<u>ATPG STRLI</u>	<u>P50007</u>	( 71)	PSRAAVLLLTSDRGLAGAFNSNSIK	17
<u>ATPG STRMU</u>	<u>P95788</u>	( 76)	IKKTAYIVITSKGLVGAYNSTILK	12

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ATPG DROME|O01666 ( 90) EPKLLIAVTS DRGLCGAVHTGVAR 33
O74754 ( 93) EGKTLMVACSSDKGLCGGIHSSISR 35
Q9NE84 ( 66) QAKAIYIPVMTNRGSCGALNSNVVK 57
O21267 ( 66) VNNKIVVPISSDRGLCGGINTNVVK 22
Q9G8R3 ( 62) DLNYLVLSITVDKSCGPHNGNVLK 100
O50141 ( 72) KNSVLLIIVIAGDRGLAGGFNTNVLK 19
O50158 ( 76) VKKTGYIVITSDKGLVGGYNSKILK 13
O67829 ( 75) ERNVDVILVTADRGLAGAFNSNVIR 19
O05432 ( 73) VKKAGYVLITADRGLAGGYNANLIR 12
Q52412 ( 70) VKKTGYLVITSDRGLAGAYNSNVLK 9
Q9ZJ02 ( 77) VKKSAYIVITSDRGLVGGYNATILK 14
Q9Z688 ( 74) SDKKLYIALTSDSGLCGGFNGAVVT 50
Q9X1U6 ( 66) GNRDLIVVITSDMGLCGSFNSEILR 25
Q9RQ80 ( 73) IKRIGLIIVSSDRGLCGSLNSNLFR 11
Q9RQ77 ( 73) TTKIGIIVISTDRGLCGSLNISLFLK 13
Q9RQ74 ( 73) VKKIGIIIIISTDRGLCGNLNVTFLK 20
Q9RGY2 ( 102) IKTTGFLVVTGDRGLVGSYNSSVIK 15
Q9RFL4 ( 73) VKRVGYLVVSTDRLCGGLNINLFLK 10
Q9RAU1 ( 75) VKKTGYLVITSDRGLVGSYNSNILK 11
Q9PR14 ( 71) KDRTLYITINSTMGLAGSYNYNVNK 40
Q9PJ20 ( 81) IKTVDLIFITADKGLCGGFNIKTLK 21
Q9PE84 ( 74) VKRIGYIVISSDRGLAGGLNNNLFR 10
Q9KNH4 ( 73) AKRVGYIIIIISTDRGLCGGLNINLFLK 12
Q9K6H4 ( 73) VKKTGYIVITSDRGLAGAYNSNLIR 9
Q9K4D4 ( 74) PSRAAVLLLTSDRGLAGAFNSNSIK 17
Q9JXQ1 ( 74) IRRVGFIITSDKGLCGGLNANVLK 14
Q9JW71 ( 74) IRRVGFIITSDKGLCGGLNANVLK 14
Q9HT19 ( 73) VKRVGYIVVSSDRGLCGGLNINLFLK 9
Q9FDR6 ( 73) GKRAAVLVVTS DRGMAGGYNHNVLK 19
Q9FAA4 ( 73) GKRAAVLVVTS DRGMAGGYNHNVLK 19
Q9CER9 ( 75) VKKTGYLVITSDRGLVGGYNSNILK 10
Q9ERA8 ( 88) KKKHLIIGVSSDRGLCGAIHSSVAK 14
Q9D9D7 ( 88) KKKHLIIGVSSDRGLCGAIHSSVAK 14
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[\[Return to top\]](#)

## Block IPB000131C

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ID  ATPase_gamma; BLOCK
AC  IPB000131C; distance from previous block=(13,21)
DE  ATP synthase gamma subunit
BL  GKR; width=11; seqs=82; 99.5%=790; strength=997
ATPG BACFI|P22482 ( 113) YGIIIMGRIGR 100

ATPG ECOLI|P00837 ( 118) IGSKGVSFENS 11

ATPG MYCGA|P33257 ( 113) VGIKLNSFLRT 49

ATPG THIFE|P41169 ( 118) VGNKGLGFLRR 24

ATPG VIBAL|P12990 ( 118) VGSKATAFFKH 28

ATP3 ARATH|Q96250 ( 147) VGEKAKAIMFR 32

ATP3 IPOBA|P26360 ( 150) LGEKAKAQLVR 20

ATPG ANASP|P12408 ( 120) VGRKAEQYFRR 18
ATPG SPIPL|P50006 ( 119) VGRKAIQHFR 15
ATPG SYNPI|Q05384 ( 120) VGRKAAQYFQR 11
ATPG SYNPI|P08450 ( 120) VGRKAGQYFQR 19
ATPG SYNPI|P17253 ( 120) VGSKAKQYFGR 14

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ATP1 ARATH	Q01908	( 169)	VGKKGNSYFLR	10
ATP2 ARATH	Q01909	( 179)	VGKKGNAFYFSR	10
ATPG CHLRE	P12113	( 153)	VGRKGAQYFAR	18
ATPG ODOSI	Q06908	( 175)	IGKKGITYFQR	12
ATPG PEA	P28552	( 170)	VGRKGNSYFNR	9
ATPG PHATR	Q41075	( 175)	VGKKGIAYFER	13
ATPG SPIOL	P05435	( 160)	IGKKGNTYFIR	16
ATPG TOBAC	P29790	( 173)	VGKKGNSYFIR	12
ATPG BACCA	P41010	( 119)	IGRVGLSFFRK	11
ATPG BACP3	P09222	( 119)	IGRVGLSFFRK	11
ATPG BUCAI	P57123	( 118)	FGLKSLSVFKL	26
ATPG BUCAP	O51873	( 118)	FGLKSLSVFKL	26
ATPG MYCGE	P47640	( 108)	LGRKNQSFWNK	34
ATPG MYCPN	Q50330	( 108)	LGRKNQSFWNK	34
ATPG PROMO	P29710	( 116)	IGKKGRDYCKK	15
ATPG RHOBL	P05436	( 119)	VGKKGREQLKR	11
ATPG RHOC	P72246	( 121)	VGKKGRDALRR	11
ATPG RHORU	P07227	( 121)	IGKKGRDGLKR	21
ATPG RICPR	O50289	( 122)	IGKKGYEALKR	21
ATPG BOVIN	P05631	( 133)	VGDKIRSILHR	24
ATPG HUMAN	P36542	( 133)	IGDKIRGILYR	18
ATPG RAT	P35435	( 108)	IGEKIKSILYR	16
ATPG KLULA	P49377	( 122)	IGDKVKGQLLR	26
ATPG YEAST	P38077	( 143)	IGDKIKMQLLR	21
ATPG ACEWO	P50005	( 114)	VGSRGRDHFRN	23
ATPG BACME	P20602	( 118)	IGRVGRDFFVK	15
ATPG BACST	P42007	( 119)	IGRVGLSFFRK	11
ATPG BACSU	P37810	( 121)	IGRVGRDFFKK	11
ATPG ENTHR	P43452	( 130)	IGGTGADFFKA	17
ATPG HAEIN	P43716	( 118)	IGSKGISFFRS	9
ATPG HELPY	P56082	( 126)	IGKKGNEYFSF	12
ATPG HELPJ	Q9ZK80	( 126)	IGKKGNEYFSF	12
ATPG MYCLE	P45824	( 119)	VGRKALNYYTF	18
ATPG MYCTU	Q10597	( 119)	VGRKAQNYYSF	19
ATPG PASMU	Q9L6B6	( 118)	IGSKSINFFQS	17
ATPG STRLI	P50007	( 116)	VGRRGLAHYNF	21
ATPG STRMU	P95788	( 121)	IGGMGSDFFRA	41
ATPG DROME	O01666	( 132)	VGDKSRILSR	18
O74754		( 137)	LGEKVRTQLLR	29
Q9NE84		( 105)	LGKRGIESLSK	32
O21267		( 111)	VGIKAKDQLQR	16
Q9G8R3		( 107)	IGRKAKFFFKK	21
O50141		( 117)	IGKKAVEYFEK	15
O50158		( 120)	IGGIGADFFKA	24
O67829		( 120)	VGRKGFQYFTK	20
O05432		( 115)	VGRKGRDFFRR	8
Q52412		( 115)	IGRVGLSFFRK	11
Q9ZJ02		( 122)	IGSVGADFFRA	13
Q9Z688		( 116)	VGQKGISYFKR	15
Q9X1U6		( 107)	VGLKAINHFKD	30
Q9RQ80		( 118)	FGLKS L P V F K L	38
Q9RQ77		( 118)	L G S K G V S Y F K S	12
Q9RQ74		( 118)	L G L K G L S F F K S	13
Q9RGY2		( 147)	V G S V G A Q F F K K	12
Q9RFL4		( 118)	I G S K G V S F F D S	19
Q9RAU1		( 120)	L G G T G A D F F K A	19
Q9PR14		( 110)	I G K K G H D F M R L	30
Q9PJ20		( 126)	I G K T G I E Y F N F	16

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Q9PE84      ( 119) IGQKASVFFRR  31
Q9KNH4      ( 118) IGSKATAFFNN  21
Q9K6H4      ( 118) IGRTGRDLLKK  27
Q9K4D4      ( 119) VGRRLAHYNF  21
Q9JXQ1      ( 119) FGSKGLMACQS  29
Q9JW71      ( 119) LGSKGLMACQS  25
Q9HT19      ( 118) IGSKGASFFRS   9
Q9FDR6      ( 118) TGKKGVDYYKF  25
Q9FAA4      ( 118) TGKKGVDYYKF  25
Q9CER9      ( 120) LGGTGADFFKA  19
Q9ERA8      ( 133) VGEKIKGILYR  18
Q9D9D7      ( 133) VGEKIKGILYR  18
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[\[Return to top\]](#)

## Block IPB000131D

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ID  ATPase_gamma; BLOCK
AC  IPB000131D; distance from previous block=(33,72)
DE  ATP synthase gamma subunit
BL  DFP; width=26; seqs=82; 99.5%=1450; strength=1161
ATPG BACFI|P22482 ( 166) DELYVWYNHFVSPITQDVTEMKLLLL  40

ATPG ECOLI|P00837 ( 166) DKLYIVSNKFINTMSQVPTISQLLPL  13
ATPG MYCGA|P33257 ( 196) DTLDRINDKFKPNISFEPGVDVIIPA 100
ATPG MYCGE|P47640 ( 158) DRICMVYTKFKNSLIQQSQLFQVFPF  33
ATPG MYCPN|Q50330 ( 158) DRICIIYTQFKNPLIQHANSFQVFPF  37
ATPG PROMO|P29710 ( 164) DEVYLIYNEFISALSTELIVKKLLPI  32
ATPG RHORU|P07227 ( 171) DVCTLVYNRFQSAISQVVTRQQIIPF  27
ATPG RICPR|O50289 ( 170) SNCIIYFNKFKNAMTQIPTKQKILPI  49
ATPG THIFE|P41169 ( 166) DVVYLVSSRFVNTMLQRATVEQLLPV  27
ATPG VIBAL|P12990 ( 166) DRLYVVFNKFVNTMVQQPTIDQLLPL  13
ATPG CHLRE|P12113 ( 201) DKVELVFTKFI SLINSNPTIQTLLPM  18

ATPG ANASP|P12408 ( 168) DRIELVYTRFVSLVSSRPVIQTLLPL  13
ATPG SPIPL|P50006 ( 167) DRVELIYTKFVSLISSRPVTQTLLPL  13
ATPG SYNP1|Q05384 ( 168) DRVELIYTKFVSLISSKPVVQTLLPL  10
ATPG SYNP6|P08450 ( 168) DRVELVYTKFSLVASNPVVQTLLPL  16
ATPG SYNY3|P17253 ( 168) DRVELIYTRFVSLISSQPVVQTLFPL  12
ATP1 ARATH|Q01908 ( 217) DKVELLYTKFVSLVKSEPVIHTLLPL  13
ATP2 ARATH|Q01909 ( 228) DKVELVYTKFVSLVKS DPVIHTLLPL  13
ATPG PEA|P28552 ( 218) DKVELLYTKFVSLVKS NPIIHTLLPL  15
ATPG SPIOL|P05435 ( 208) DKVEMLYTKFVSLVKS DPVIHTLLPL  16
ATPG TOBAC|P29790 ( 221) DKVELLYTKFVSLVKS EPVIHTLLPL  13

ATPG BACCA|P41010 ( 167) DELYMYYNHYVSAIQQEVTERKLLPL  17
ATPG BACP3|P09222 ( 167) DELYMYYNHYVSAIQQEVTERKLLPL  17

ATPG BUCAI|P57123 ( 166) DKIFIAYNKFHNKMSQYPTITQLLPF  23
ATPG BUCAP|O51873 ( 166) DRLFIAYNKFHNKLSQYPKISQLLPL  17

ATPG RHOBL|P05436 ( 169) DVVTIFYNRFQSVISQVPTAQQVIPA  24

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ATPG RHOCAL	P72246	( 171)	DVATIFFSVFQSVISQVPTAKQVIPA	49
ATPG ODOSE	Q06908	( 222)	DAVELLYTKFISLIASSPSARTLIPF	18
ATPG PHATRL	Q41075	( 222)	DAVELLYTKFVSLIASSPSIRTLVPF	21
ATPG ARATHL	Q96250	( 194)	DALRIVYNKFHSSVVAFLPTVSTVLSP	30
ATPG IPOBAL	P26360	( 197)	DALRIVFNKFQSVVSFVPTMSTVLSP	25
ATPG BOVINL	P05631	( 181)	DEGSIIFNFRSVISYKTEEKPIFSL	22
ATPG HUMANL	P36542	( 181)	DEGSIIFNKFRSVISYKTEEKPIFSL	22
ATPG RATL	P35435	( 156)	DEGSIIFNQFKSVISYKTEEKPIFSF	21
ATPG KLULAL	P49377	( 179)	DPISSLSFEPSPNKPVFNAAAIEQSPS	78
ATPG YEASTL	P38077	( 201)	DPVSSLSFEPSEKPIFNAKTIEQSPS	90
ATPG ACEWOL	P50005	( 162)	DEVYIAYTKFVSTITQHAQMMKLLPL	17
ATPG BACME	P20602	( 166)	DELYLYYNHFINTISQEVTEKKLLPL	11
ATPG BACSTL	P42007	( 167)	DELYMYYNHYVSAIQEVTERKLLPL	17
ATPG BACSL	P37810	( 169)	DELHLVYNHFVSAITQEVTEKKLLPL	10
ATPG ENTHRL	P43452	( 178)	DELYVCYNHHINSLTSQFRVEKMLPI	20
ATPG HAEINL	P43716	( 166)	DAVYIAYNKFNVTMSQKPVVQQLVPL	16
ATPG HELPYL	P56082	( 174)	DKVIIHNGFKNMITQEIRVKTILPI	23
ATPG HELPJL	Q9ZK80	( 174)	DKVIIHNGFKNMITQEIRVKTILPI	23
ATPG MYCLEL	P45824	( 173)	DELHIVFTEFKSMLSQSTKARRMAPM	23
ATPG MYCTUL	Q10597	( 180)	DELHIVYTEFKSMLSQSAEAHRIAPM	20
ATPG PASMUL	Q9L6B6	( 166)	DVVYLVYNKFINTMSQKPVLEKLIPL	15
ATPG STRLL	P50007	( 168)	DELHIVYTEFVSMMTQTAVDSRLLPL	18
ATPG STRMUL	P95788	( 169)	DELYVCYSHHINSLTSQVRVEKMLPI	19
ATPG DROMEL	O01666	( 180)	TEGKIVYNRFKSVVSYQCSTLPIFSG	58
O74754		( 185)	DRIVLVYNKFASAVSFETVMKNLYTT	69
Q9NE84		( 153)	DRVHVI FHRCVSAGSQKQCYYNIPSY	91
O21267		( 157)	DTCYLVYNQFRSVLTQNVIESKIASR	36
Q9G8R3		( 153)	DRFYII FNRFYSAFTQKVSYYDVCSF	59
O50141		( 165)	DAVELVYTTTFVSVMTQEPQHLRILPV	34
O50158		( 168)	DELYVCYNHHVNSLTSQVRVQQLPL	16
O67829		( 169)	DRVYLINNEMVTRASYKQVRVFLPF	84
O05432		( 163)	DEVNLTINRFYSPIRQVPMVERLLPI	37
Q52412		( 163)	DELYMYYNHYVSAIQEVTERKLLPL	17
Q9ZJ02		( 170)	DELYVCYNHHVNSLTSQMRVEQMLPI	24
Q9Z688		( 164)	GEVHVIYTQFLSTVNQKVEVKVLPI	35
Q9X1U6		( 152)	ARVRVIFSRFKNVLIQRPEVHELLPI	35
Q9RQ80		( 166)	DKIFIAYNEFHKNMSQYPKIIQLLPL	19
Q9RQ77		( 166)	DKLFLSYNQFKNTLVYIPVIMQLLPL	27
Q9RQ74		( 166)	DRLFLAYNKFKSTLIQIPSIQLLPL	16
Q9RGY2		( 195)	DQLYVCYTHHVNSLSSAFRVEKMLPI	28
Q9RFL4		( 166)	DKLYIVSNKFINTMSQVPTISQLLPL	13
Q9RAU1		( 168)	DELYVCYNHHVNSLVSEARMEKMLPI	18
Q9PR14		( 160)	NKICIIYTKFINAITFEVSVIDVLPF	36
Q9PJ20		( 174)	DEVILVHNGYKNMITQELKINHILIPV	41
Q9PE84		( 167)	DRVYLVYNRFINTMVQKASFDQLLPL	19
Q9KNH4		( 166)	DRLYLVFNQFVNTMVQKPKIDQLLPL	14
Q9K6H4		( 166)	DELYIWNHNFVSPKQDVTEKKVLPL	18
Q9K4D4		( 171)	DELHIVYTEFVSMMTQTAVDSRLLPL	18
Q9JXQ1		( 167)	DRIHLVYSGFVNTMRQEPRMEVLLPI	19
Q9JW71		( 167)	DRIHLVYSGFVNTMRQEPRMEVLLPI	19
Q9HT19		( 166)	DRLFVVSNNKFVNTMTQKPTVEQLIPL	14
Q9FDR6		( 186)	DQVHVYVTEFISMLTQNPVVHQLLPV	16
Q9FAA4		( 186)	DQVHVYVTEFISMLTQNPVVHQLLPV	16
Q9CER9		( 168)	DELYVCYNHHVNSLVSDARMEKMLPI	18
Q9ERA8		( 181)	DEGSIIFNQFKSVISYKTEEKPIFSL	21
Q9D9D7		( 181)	DEGSIIFNQFKSVISYKTEEKPIFSL	21

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[\[Return to top\]](#)

## Block IPB000131E

ID	ATPase_gamma; BLOCK		
AC	IPB000131E; distance from previous block=(13,74)		
DE	ATP synthase gamma subunit		
BL	NQE; width=53; seqs=82; 99.5%=2428; strength=1518		
ATPG MYCGA	P33257	( 235)	LIESKVCEYASRRNAMDTAAKNADDLYNKYKLLYNQLRQAKITQEINEIVAGA 23
ATPG PROMO	P29710	( 226)	ILENTASEHSARKNAMKNATDNAEDMIKDLTLQYNRERQAAITQEISEIVSGA 15
ATPG RICPR	O50289	( 233)	LLQNIVSEEGARMTAMENATNNANDLISKLVKLNRSRQTIITTELIEIIAGA 31
ATPG THIFE	P41169	( 233)	VIEHLACEQSARMVAMKSASDNAKRMVDDLQLAYNKARQAAITQEIAEISAGA 23
ATPG CHLRE	P12113	( 301)	LQEALASELAARMNAMNNASDNAKELKKGLTVQYNKQRQAKITQELAEIVGGA 15
ATPG ANASP	P12408	( 259)	LQESAASELAARMTAMSNASENAGELIKSLSYNKARQAAITQELLEVVGA 13
ATPG SPIPL	P50006	( 258)	WQESTASELAARMTAMSNASDNASDLVKTLTSLYNKARQASITQELLEVVGA 14
ATPG SYNPI	Q05384	( 259)	LQEAAAASELAARMTAMNNASDNAQTTLIGTLTSLYNKARQAAITQELLEVVGA 14
ATPG SYNPI	P08450	( 259)	LQEAAAASELAARMTAMNSASDNANALVGQTLVYNKARQAAITQELLEVVGA 13
ATPG SYNPI	P17253	( 259)	LQESAASELAARMTAMSNASDNAGQLIGTLTSLYNKARQAAITQELLEVVGA 14
ATPG BACCA	P41010	( 231)	LLDAKASEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGR 10
ATPG BACFI	P22482	( 233)	LLDAKASEFGARMTAMSAATDNASALIEELTLKFNRRARQAAITQEITEIVGGA 12
ATPG BACP3	P09222	( 230)	LLDAKASEHAARMTAMKNATDNANELIRTLTSLYNRARQAAITQEITEIVAGA 8
ATPG BUCAI	P57123	( 232)	I LENIASEHAARMIAMKTATDNSGNRIKELQLVYNKVRQANITQELNEIVSGA 13
ATPG BUCAP	O51873	( 233)	L LENIASEQAARMVAMKTATDNSGNRIKELQLIYNKVRQANITQELTEIVAGA 12
ATPG ECOLI	P00837	( 232)	VVENLASEQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGA 12
ATPG VIBAL	P12990	( 233)	VVENLACEQAARMIAMKAATDNATNLIDDLVYNKARQAAITQELSEIVGGA 13
ATPG MYCGE	P47640	( 226)	LVETKLCESASRQNAMEAATKNAKDLLDKYTLQFNKLRQNSITEEIIIEVIGGM 27
ATPG MYCPN	Q50330	( 226)	LVETKLCESASRQNAMEAATKNAKDLLDKYTLQFNKLRQNSITQEIIIEIIGGI 26
ATPG RHOBL	P05436	( 231)	LLENASEQGARMSAMDNATRNAGDMINKLTIQYNRSRQAAITKELIEIISGA 10
ATPG RHOCB	P72246	( 235)	LLENNASFNQAQMSAMDNATRNAGDMIDRLTIEYNRSRQAAITKELIEIISGA 25
ATPG RHORU	P07227	( 244)	MLESFASEQGARMTAMDNATRNAGDMIKKLSLTYNRTRQAQITKELIEIISGA 11
ATP1 ARATH	Q01908	( 317)	LQESLASELAARMSAMSSASDNASDLKKSLSMVYNRKRQAKITGEILEIVAGA 15
ATP2 ARATH	Q01909	( 328)	LQESLASELASRMNAMSNATDNARELKKNLTMAYNRARQAKITGELLEIVAGA 15
ATPG PEA	P28552	( 318)	LQESLASELAARMSAMSSAFDNASELKTDLTRVYNRATQAKITGEILEIVAGD 37
ATPG SPIOL	P05435	( 308)	LQESLASELAARMTAMSNATDNANELKKTLISINYNRARQAKITGEILEIVAGA 12
ATPG TOBAC	P29790	( 321)	LQESLASELAARMSAMSSATDNATELKKNLRSVYNRQRQAKITGEILEIVAGA 12
ATPG ODOSI	Q06908	( 314)	LQESVASELAARMQSMQSASDNAGDLAKRLSTEYNRARQAAVTQEILEIVSGA 23
ATPG PHATR	Q41075	( 314)	LQESVASELAARMQSMQSASDNAGSLAKQLNLEYNRARQAAVTQELLEIISGA 23
ATP3 ARATH	Q96250	( 266)	VLENACSEMGAARMSAMSSSRNAGEMLDRLTLTYNRTRQASITTELIEIISGA 18
ATP3 IPOBA	P26360	( 269)	VLENACSEQGARMSAMSSSRNAGEMLDRLTLTYNRTRQASITTELIEIISGA 17
ATPG BOVIN	P05631	( 242)	LKESTTSEQSARMTAMDNASKNASEMIDKLTTLTFNRTRQAVITKELIEIISGA 10
ATPG HUMAN	P36542	( 242)	LKESTTSEQSARMTAMDNASKNASEMIDKLTTLTFNRTRQAVITKELIEIISGA 10
ATPG RAT	P35435	( 217)	LKESTTSEQSARMTAMDNASKNASDMIDKLTTLTFNRTRQAVITKELIEIISGA 10
ATPG KLULA	P49377	( 233)	MAEGYAAEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGA 22
ATPG YEAST	P38077	( 255)	MAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGA 23
ATPG ACEWO	P50005	( 245)	MIESAASEQGARRTAMESATTNANEMIDGLTLQYNRVQAPITQEISEIVGGA 18
ATPG BACME	P20602	( 229)	LLDGKASEHAARMTAMKSATDNAKDLINNLTLSYNRARQAAITQEITEIVGGA 9
ATPG BACST	P42007	( 231)	LLDAKASEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGR 10
ATPG BACSU	P37810	( 234)	LLDSKASEHAARMTAMKNATDNAKELIDSLSLSYNRARQAAITQEITEIVGGA 8
ATPG ENTHR	P43452	( 244)	IVDAKTAETHAAGMTAMKTATDNAATIIDDLTVSYNRARQGAITQEITEIVAGA 20

ATPG_HAEIN P43716	( 234 )	VVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA	11
ATPG_HELPY P56082	( 245 )	LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV	16
ATPG_HELPJ Q9ZK80	( 245 )	LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV	16
ATPG_MYCLE P45824	( 239 )	MLESAASELASRQRAMKSATDNADDLIKALTLEANRERQAQITQEISEIVGGA	14
ATPG_MYCTU Q10597	( 246 )	LLESAASELASRQRAMKSATDNADDLIKALTLMANRERQAQITQEISEIVGGA	16
ATPG_PASMU Q9L6B6	( 234 )	AVENLASEQAARMVAMKAATDNAGNLINELQLVYNKARQASITNELNEIVAGA	13
ATPG_STRLI P50007	( 238 )	LLQSAASKHAATRRAMKSATDNAGELINTLSRLANAARQAQITQEISEIVGGA	22
ATPG_STRMU P95788	( 236 )	IIDAKTAEHAAGMTAMQTATDNADKVIEDLTKLYNRVRQAQITQEITEIVAGA	17
ATPG_DROME O01666	( 241 )	MKEGACSEQSSRMTAMDNASKNAGEMIDKLTTLTFNRTRQAVITRELIEIISGA	14
O74754	( 245 )	MAEAHCSEMSSRRNAMENASKSAGDMINKFSIQYNRQRQASITNELIDIVTGA	38
Q9NE84	( 228 )	VCENELSEQAARLVAVEGQLSNISTLQQKTSSLYNKTRQSSITSSSLIEIISAM	100
O21267	( 221 )	LIENVTSEQGARMNAMDNAAKNAGEMIDKLTLYNKARQASITSELIEIISCA	18
Q9G8R3	( 232 )	LEENEYSALGARATAMNNATKNVSELIDRLRLSYNKARQETITNELIEIVSCV	42
O50141	( 229 )	IVDSFASEQAARRTAMESASDNANEMIEKLSLLYNRARQAQITQEITEISSA	19
O50158	( 235 )	IVDAKTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAQITQEITEIVAGA	11
O67829	( 233 )	MVESNAAEHFARMIAMDNATKNAEDLIRQWTLVFNKARQEAITTELIDITNAV	41
O05432	( 226 )	LLEAKASEHGARTAMDNATKNAEMIDKFTLSFNRRARQAQITNEIVEIVAGA	13
Q52412	( 226 )	LLDAKASEHAARMTAMKNATDNANELIRTLTSLYNRARQAQITQEITEIVAGA	8
Q9ZJ02	( 237 )	IIDAKTAENAAGMTAMQTATDNAKKVISDLTIQYNRARQAQITQEITEIVAGA	13
Q9Z688	( 226 )	LLNSKASEQASRMSSMDSATKNANDLLDALNIKYNRIQSAITQEITEIVGGA	27
Q9X1U6	( 213 )	MFQTKIGEYYARQONAMKNATDNAQEVIRELTLAYNKARQASITQELIEIVTGA	33
Q9RQ80	( 232 )	ILENIASEHAARMAMKTATENSTERIKELKLLYNKVRQATITQELTEIISGA	19
Q9RQ77	( 232 )	ILENTCEQASRMISMKQATDNSEDLIKLRILYNKARQDNITQELTEIISGA	23
Q9RQ74	( 231 )	SLENTTSEQAARMIAMKQATDNSKDLIRELQIIYNKARQDNITQELTEIVSGA	19
Q9RGY2	( 264 )	ILDAKTAEHASSMTAMQSATDNANDLVSNTTKLNRARQAQITTEITEIISGA	23
Q9RFL4	( 232 )	VVENLASEQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGA	12
Q9RAU1	( 234 )	IVDAKTAEHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGA	14
Q9PR14	( 232 )	LIESKISENASRRNAMDAATKNAKALAENYKLIYNTLRQGKITREITEIVAGS	29
Q9PJ20	( 238 )	LIDSLAAEHSARMQAMDNATNNAKARVKQLNLAYNKARQESITTELIEIISGV	16
Q9PE84	( 232 )	MLENIASEHAARMVAMKAASDNANKLIGTLQLVYNKARQAQITQEISEIVGGA	11
Q9KNH4	( 233 )	VVENLACEQAARMVAMKAATDNASNLIIDDLQLVYNKARQAQITQELSEIVGGA	10
Q9K6H4	( 229 )	LLDAKASEFAARMTAMSAATDNATNLIDELTSLYNRARQAQITQEITEIVGGA	10
Q9K4D4	( 241 )	LLQSAASKHAATRRAMKSATDNAGELINTLSRLANAARQAQITQEISEIVGGA	22
Q9JXQ1	( 236 )	LSDNMASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAQITTELSEIVAGA	14
Q9JW71	( 236 )	LSDNMASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAQITTELSEIVAGA	14
Q9HT19	( 231 )	VVENNACEQAARMIAMKNATDNAGELISDLQLIYNKARQAQITQEISEIVGGA	11
Q9FDR6	( 263 )	FLEAAAAESASRRNAMKSATDNATELVKDLRSRVANQARQAQITQEITEIVGGA	16
Q9FAA4	( 263 )	FLEAAAAESASRRNAMKSATDNATELVKDLRSRVANQARQAQITQEITEIVGGA	16
Q9CER9	( 234 )	IVDAKTAEHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGA	14
Q9ERA8	( 242 )	LKESTTSEQSARMTAMDNASKNASDMIDKLTTLTFNRTRQAVITKELIEIISGA	10
Q9D9D7	( 242 )	LKESTTSEQSARMTAMDNASKNASDMIDKLTTLTFNRTRQAVITKELIEIISGA	10

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## COBBLER sequence (region containing Blocks only)

To do a BLAST search, copy the cobbler sequence below then click on a BLAST link

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COBBLER sequence:

```
>IPB000131 ATPG_BACME|P20602 from 1 to 285 with embedded consensus blocks
masLKEIKRRIKSVKNTQKITKAMKMVAAAKLRKAeqnaksfvpymekiqevvssvalgsrgashpmltarsVKKTLYIV
ITSDRGLCGGYNSNVIKkvsqaeerhqspsdeygviaIGKKGMSYFKRRgipvlleitgladqpafadiqqiasqtvqmf
```

adgtfDEVYIIYNKFVNAISQEPTVKQLLPLtdlqpsgklvgyefepsqeeilevllpqaesliyyggLLESKASEHAAR  
MTAMENATDNAGDLIKKLTlVYNRARQAAITQELIEIVSGAaale

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[MetaFam IPB000131](#)

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S2	7	S1/2000:2003
S3	14	S1 NOT S2

?t s3/9/1

3/9/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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**Identification and characterization of the putative transcription-repair-coupling factor gene (trcL) of *Listeria monocytogenes*.**

AUTHOR: Zheng W; Kathariou S

AUTHOR ADDRESS: Univ. Hawaii, Honolulu, HI\*\*USA

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 97 (0):p362 1997

CONFERENCE/MEETING: 97th General Meeting of the American Society for Microbiology Miami Beach, Florida, USA May 4-8, 1997

ISSN: 1060-2011

RECORD TYPE: Citation

LANGUAGE: English

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Physiology

BIOSYSTEMATIC NAMES: Endospore-forming Gram-Positives--Eubacteria, Bacteria; Enterobacteriaceae--Eubacteria, Bacteria; **Pasteurellaceae** --Eubacteria, Bacteria; Regular Nonsporing Gram-Positive Rods--Eubacteria, Bacteria

ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); regular nonsporing gram-positive rods (Regular Nonsporing Gram-Positive Rods); *Bacillus subtilis* (Endospore-forming Gram-Positives); *Escherichia coli* (Enterobacteriaceae); ***Haemophilus influenzae*** ( ***Pasteurellaceae*** ); *Listeria monocytogenes* (Regular Nonsporing Gram-Positive Rods

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms

MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; nucleotide sequence


MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster; CHARACTERIZATION ; CHEMICAL COORDINATION; COLD STRESS; COLD STRESS RESPONSE GENE; FOOD CONTAMINANT; IDENTIFICATION; IN FRAME DELETION MUTANT; LTRA GENE; LTRB GENE; LTRC GENE; MOLECULAR GENETICS; TRANSCRIPTION-REPAIR- **COUPLING FACTOR** ; TRANSCRIPTION-REPAIR- **COUPLING FACTOR** GENE; TRCL GENE; TRCL GENE PRODUCT

CONCEPT CODES:

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines  
10064 Biochemical Studies-Proteins, Peptides and Amino Acids  
10616 External Effects-Temperature as a Primary Variable-Cold (1971- )  
23010 Temperature: Its Measurement, Effects and Regulation-Thermoadaptation  
31000 Physiology and Biochemistry of Bacteria  
31500 Genetics of Bacteria and Viruses  
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals

BIOSYSTEMATIC CODES:

06702 Enterobacteriaceae (1992- )  
06703 **Pasteurellaceae** (1992- )  
07810 Endospore-forming Gram-Positives (1992- )  
07830 Regular Nonsporing Gram-Positive Rods (1992

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## NiceSite View of PROSITE: PDOC00138 (documentation)

### ATP synthase gamma subunit signature

PROSITE cross-reference(s)	
<u>PS00153; ATPASE GAMMA</u>	
Documentation	
<p>ATP synthase (proton-translocating ATPase) (EC 3.6.3.14) [1,2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis. As a signature pattern to detect ATPase gamma subunits, we used a 14 residue conserved segment where the last amino acid is found one to three residues from the C-terminal extremity.</p>	
Description of pattern(s) and/or profile(s)	
<b>Consensus pattern</b>	[IV]-T-x-E-x(2)-[DE]-x(3)-G-A-x-[SAKR]
<b>Sequences known to belong to this class detected by the pattern</b>	ALL, except for pea chloroplast gamma and two Bacillus species gamma.